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FIG. :

TGGGCACAGC CACC	CTGTTG GTAGT	CCAGG GGCCA	AGCCCA CTGAGCT	GGC ATATCAGCTG	śΰ
GTGGCCCCGT TGGA	ACTCGGC CCTAG	GGAAC GGCGG	GCG ATG GGA GC Met Gly Al 1	G CCC CGG ATC : a Pro Arg Ile	113
TCG CAC AGC CTT Ser His Ser Leu 10	ı Ala Leu Leu	CTC TGC TG Leu Cys Cy 15	GC TCC GTG CTC ys Ser Val Leu	AGC TCC GTC Ser Ser Val	157
TAC GCA CTG GTG Tyr Ala Leu Val 25	GAT GCC GAT . Asp Ala Asp	GAT GTC AT Asp Val II	TA ACG AAG GAG Le Thr Lys Glu 35	GAG CAG ATC C	2:_
ATT CTT CTG CGC Ile Leu Leu Arg 40	: AAT GCC CAG ASN Ala Gln 45	GCC CAG TG Ala Gln Cy	GT GAG CAG CGC ys Glu Gln Arg 50	CTG AAA GAG 2 Leu Lys Glu	259
GTC CTC AGG GTC Val Leu Arg Val 55	CCT GAA CTT Pro Glu Leu 60	GCT GAA TO Ala Glu Se	T GCC AAA GAC er Ala Lys Asp 65	TGG ATG TCA Trp Met Ser 70	307
AGG TCT GCA AAG Arg Ser Ala Lys	ACA AAG AAG Thr Lys Lys 75	Glu Lys Pr	T GCA GAA AAG TO Ala Glu Lys 10	CTT TAT CCC 3 Leu Tyr Pro 85	355
CAG GCA GAG GAG Gln Ala Glu Glu 90	Ser Arg Glu	GTT TOT GA Val Ser As 35	AC AGG AGC CGG BD Arg Ser Arg	CTG CAG GAT 4 Leu Gln Asp 100	103
GGC TTC TGC CTA Gly Phe Cys Leu 105	. COT SAG TEG Pro Glu Trp	HAC HAC HT HASD HASD II 110	DDT DDT DTG TG dTC eys Tak a. 115	COT GOT GGA 4 Pro Ala Gly	. : .
GTG CCC GGC AAG Val Pro Gly Lys 120	GTG GTG GCC Val Val Ala 125	GTG CCC TG Val Pro Cy	C CCC GAC TAC S Pro Asp Tyr 130	TTC TAC GAC 4 Phe Tyr Asp	Ģ Ģ
TTC AAC CAC AAA Phe Asn His Lys 135	GGC CGA GCC Gly Arg Ala 140	TAT CGG CG Tyr Arg Ar	C TGT GAC AGC G Cys Asp Ser 145	AAT GGC AGC 5 Asn Gly Ser 150	47
TGG GAG CTG GTG Trp Glu Leu Val	CCT GGG AAC Pro Gly Asn 155	AAC CGG AC Asn Arg Th 16	r Trp Ala Asn	TAC AGC GAA 5 Tyr Ser Glu 165	95
TGT GTC AAG TTT Cys Val Lys Phe 170	Leu Thr Asn	GAG ACC CG Glu Thr Ar 175	g GAA CGG GAA g Glu Arg Glu	GTC TTT GAT 64 Val Phe Asp 180	43

			185				C ACT	190	913		. 36	E 11	.e So 19	er L 95	eu (Gly	Ser	
	20	0				_	ATT Ille 205		327	- 2 -	110	21	g Al	g L	au E	lis	cys	739
21.	5			-		220				2.16	225	. se:	ב פח	e Me	et I	æu	Arg 230	7 87
					235		AAG Lys		via	240	Leu	1 171	r Se	r Gl	y V 2	al 45	Ser	835
		-		250			ATC Ile	- • • •	135	GIU	GIU	Let	1 Ar	g Al 26	a Pi O	he	Thr	883
		2	65				AAG Lys	270	314	rne	AGI	GIĄ	27:	s Ar	g Va	11 .	Ala	931
	280)				-1-	TTC Phe 285	Leu	4	inr	ASN	290	ТУХ	Trj	P II	Le 1	Leu	979
295			-, .		-1-	300	CAC His	ser	_3 u	ile	Phe 305	Met	Ala	Phe	Ph	e 5	Ser 310	1027
	•			- , -	315		G GT Gly	=	• • • •	120	FUE	GIY	Trp	Gly	Le 32	u P 5	ro	1075
			3	30				•	2.3	31	.ug	Ala	Thr	Leu 340	Al	a A	sn	1123
		3 4	5	•				250	·-! .	-SN	rys	Lys	Trp 355	Ile	Ile	3 G.	ln	1171
	360						ATT (Ile \ 365		4 £ £	, 116	riie	37 0	Leu	Phe	Ile	A A S	sn	1219
ATA Ile 375	ATC Ile	AG	A G g V	TC (GCT Ala 9	ACT 3 Thr 1	AA C	TC C A US	ug (GAG A Glu (85	ACC . Thr .	A A T Asn	GCA Ala	G GG Gly	Ar Ar 39	g	1267

Fig. :

9,3	G AC Asp	1441	λty	395	GIN	TYE	Arg	rys	400	Leu	Lys	Ser	Thr	Leu 405	Val	1315
CTC Leu	ATG Met	CCG Pro	CTA Leu 410	TTT Phe	GGG Gly	GTG Val	CAC His	TAC Tyr 415	ATC Ile	GTC Val	TTC Phe	ATG Met	GCC Ala 420	ACG Thr	CCG Pro	1353
TAC Tyr	ACA Thr	GAA Glu 425	GTA Val	TCA Ser	G GG Gly	ATT Ile	CTT Lau 430	TGG Trp	CAA Gln	GTC Val	CAA Gln	ATG Met 435	CAC His	TAT Tyr	GAA Glu	1411
ATG Met	CTC Leu 440	TTC Phe	AAT Asn	TCA Ser	TTC Phe	CAG Gln 445	GGA Gly	TTT Phe	TTC Phe	GTT Val	GCC Ala 450	ATT Ile	A TA Ile	TAC Tyr	TGT Cys	1459
TTC Phe 455	TGC Cys	AAT Asn	GGA Gly	GA G Glu	GTA Val 460	CAA Gln	GCA Ala	G AG Glu	ATC Ile	AAG Lys 465	AAG Lys	TCA Ser	TGG Trp	AGC Ser	CGA Arg 470	1507
TGG	ACC Thr	C TG Leu	GCC Ala	TTG Leu 475	GAC Asp	TTC Phe	AAG Lys	cg g Arg	AAG Lys 480	GCC Ala	CGG Arg	AGT Ser	Gly	AGC Ser 485	A GT S er	1555
ACC Thr	TAC Tyr	SEL	TAT Tyr 490	G GC Gly	CCC Pro	ATG Met	Val	TCA Ser 495	CAT His	ACA Thr	A GT Ser	Val	ACC . Thr . 500	AAT Asn	G TG Val	1603
G GA Gly	CCT Pro	CG A Arg 5 05	G GG Gly	G GC Gly	TGG Trp	Pro	TGT Cys 510	c cc Pro	TCA Ser	GCC Ala	Leu	GAC Asp 515	TAGC	rccr	GG	1652
GGCT	GGAG	CC A	GTGC	CAAT	G GC	CATC.	ACCA	GTT	scct	GGC	TATG'	TGAA	GC A	rggt:	TCCAT	1712
TTCT	GAGA	AC T	CATT	GCCT	T CA	TCTG	GCCC	AGA	GCCT	GGC	ACCA	AAGA:	rg ac	CGGG:	TATCT	1775
CAAT	GGCT	ct G	Gact	TTAT	G AG	CCAA	TGGT	TGG	GGAA	CAG	cccc	crcci	AC TO	crs	GAGGA	1332
GGAG	AGAG.	AG A	CAGT	CATG'	r ga	CCCA	TATC									1862

TGG	GCAC	CAGC	CACC	CTGI	TG G	TAGT	CCAG	G GG	CCAG	iccc;	CTO	GAGC:	rggc	ATA	ICAGCT	G 60
GTG	GCCC	CGT	TGGA	CTCG	GC C	CTAG	ggaa	C GG	CGGC	G AT	G GG et Gl	A GO	CG CC	CC CC	GG ATC FG Ile 5	115
TCG Ser	CAC His	AGC Ser	CTI Leu 10	Ala	TTG Leu	CTC Leu	c rc Leu	TGC Cys 15	TGC Cys	TCC Ser	GTG Val	CTC Lev	AGC Ser 20	Sez	GTC Val	163
TAC	GCA Ala	CTG Leu 25	G TG Val	GAT Asp	GCC Ala	GAT Asp	RAT Asp 30	G TC Val	ATA Ile	ACG Thr	AAG Lys	GAG Glu 35	Glu	CAG Glr	ATC Ile	211
ATT Ile	CTT Leu 40	Leu	CGC Arg	AAT Asn	GCC Ala	CAG Gln 45	GCC Ala	CAG Gln	TG T Cys	GAG Glu	CAG Gln 50	CGC Arg	CTG Leu	A AA Lys	GAG Glu	25 9
GTC Val 55	CTC Leu	AGG Arg	GTC Val	CCT Pro	GAA Glu 60	CTT Leu	GCT Ala	GAA Glu	TCT Ser	GCC Ala 65	A AA Lys	G AC Asp	TGG Trp	ATG Met	TCA Ser 70	₹
AGG Arg	TCT Ser	GCA Ala	AAG Lys	ACA Thr 75	AAG Lys	AAG Lys	GAG Glu	AAA Lys	CCT Pro 80	GCA Ala	GAA Glu	A AG Lys	CTT Leu	TAT Tyr 85	CCC Pro	35 5]
CAG Gln	GCA Ala	G AG Glu	GAG Glu 90	TCC Ser	AGG Arg	GAA Glu	GTT Vai	TOT Ser 35	GAC Asp	AGG Arg	AGC Ser	cgg Arg	CTG Leu 100	Gln	GAT Asp	40 3
3GC 31γ	TTC Phe	TGC Cys 103	CTA Lau	cor	GAG Glu	TGG	JAC ST 11	AC sn	ATT	GTG Val	TGC Cys	TGG Trp 115	CCT Pro	GCT Ala	G GA Gly	451
GTG Val	CCC Pro 120	GGC Gly	AAG Lys	GTG Val	GTG Val	GCC Ala 125	375 711	700 720	TGC Cys	CCC Pro	GAC Asp 130	TAC Tyr	TTC Phe	TAC Tyr	G AC Asp	499
TTC Phe 135	AAC Asn	CAC His	AAA Lys	GGC Gly	CGA Arg 140	GCC Ala	TAT Tyr	og g A rg	CG C Arg	TGT Cys 145	G AC Asp	AGC Ser	AAT Asn	G GC Gly	AGC Ser 150	547
Trp	G AG Glu	CTG Leu	G TG Val	CCT Pro 155	G GG Gly	AAC Asn	AAC Asn	arg Arg	ACA Thr 160	TGG Trp	GCG Ala	AAT Asn	Tyr	AGC Ser 165	G AA Glu	595
T GT Cys	GTC Val	Lys	TTT Fhe 170	CTG Leu	ACC Thr	AAC Asn	Glu	ACC Thr 175	cgg Arg	G AA Glu	c gg Arg	Glu	GTC Val 180	TTT Phe	G AT A sp	643

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295		_			300			_eu	176	30 5	Met	Ala	Phe	Phe	TCT Ser 310	1027 © 2
		-	TAT	CTC Leu J15	TSG	GGT Gly	TTC Phè	ACA Thr	TTA Lau	Sys	GGC Gly	TGG	G GC Gly	CTC Leu 325	CCT Pro	1075
Ala	GTG Val	Phe	Val 330		Val			335	∵aı	arg.	Ala	Thr	Leu 340	Ala	Asn	1123
ACT	GAG Glu	TGC Cys 345	TGG	GAC Asp	CTG Leu	AGT Ser	TCG Ser 350	G GG Gly	AAT Asn	AAG Lys	A AA Lys	TGG Trp 355	ATC Ile	ATA Ile	CAG Gln	1171
GTG Val	CCC Pro 360	ATC Ile	CTG Leu	GCA Ala	GCT Ala	ATT Ile 365	GTG (Val	GT G Val	AAC Asn	Pue	ATT Ile 370	CTT Leu	TTT Phe	ATC Ile	A AT Asn	1219
ATA Ile 375	ATC Ile	AG A Arg	G TC Val		GCT Ala 380	ACT Thr	AAA (Lys)	CTC Leu .	arg (GAG Glu 385	ACC Thr	A AT Asn	G CA Ala	G GG Gly	AGA Arg 390	1267

TGT Cys	GAC Asp	ACG	AGG Arg	CAA Gln 395	CAG Gln	TAT Tyr	AGA Arg	AAG Lys	CTG Leu 400	CTG Leu	AAG Lys	TCC Ser	ACG Thr	CTA Leu 405	GTC Val	1315
CTC Leu	ATG Met	CCG Pro	CTA Leu 410	TTT Phe	G GG Gly	GTG Val	CAC His	TAC Tyr 415	ATC Ila	GTC Val	TTC Phe	ATG Met	GCC Ala 420	ACG Thr	Pro	1363
TAC Tyr	ACA	GAA Glu 425	GTA Val	TCA Ser	G GG Gly	ATT	CTT Leu 430	TCG	CAA Gln	GTC Val	CAA Gln	ATG Met 435	CAC His	TAT Tyr	GAA Glu	1411
ATG Met	CTC Leu 440	TTC	AAT Asn	TCA Ser	TTC Phe	CAG Gln 445	GGA Gly	TTT	TTC Phe	GTT Val	GCC Ala 450	ATT Ile	ATA Ile	TAC Tyr	TGT Cys	1459
TTC Phe 455	TGC Cys	AAT Asn	G GA Gly	GA G Glu	GTA Val 460	CAA Gln	GCA Ala	GAG Glu	ATC Ile	AAG Lys 465	AAG Lys	TCA Ser	TGG Trp	AGC Ser	CGA Arg 470	1507
TGG Trp	ACC Thr	CTG Leu	GCC Ala	TTG Leu 475	GAC Asp	TTC Fhe	AAG Lys	cgg	AAG Lys 480	GCC Ala	CGG Arg	AGT Ser	GGC Gly	AGC Ser 485	AGT Ser	1555
ACC Thr	TAC Tyr	AGC Ser	TAT Tyr 490	Gly	CCC Pro	ATG Met	GTG Val	TCA Ser 495	His	ACA Thr	AGT Ser	GTC Val	ACC Thr 500	Asn	G TG Val	1603
G GA Gly	CCT	CGA Arg 505	G GG Gly	G GG Gly	CTG Leu	GCC Ala	TTG Leu 510	TCC Ser	CTC Leu	AGC Ser	Pro	CGA Arg 515	CTA Leu	GCT Ala	CCT Pro	1651
GGG Gly	GCT Ala 520	GGA Gly	GCC Ala	AGT Ser	GCC Ala	AAT Asn 525	GGC Gly	CAT	CAC	CA G Gln	TTG Leu 530	CCT Pro	GGC Gly	TAT Tyr	GT G Val	1699
AAG Lys 535	CAT	GGT Gly	TCC Ser	ATT Ile	Ser 540	GAG Glu	AAC Asn	ion Jer	Lau	CCT Pro 5 45	TCA Ser	T CT S er	GGC Gly	Pro	GAG Glu 5 50	1747
Pro	GGC Gly	ACC Thr	A AA Lys	GAT Asp 555	Asp	G GG Gly	TAT Tyr	CTC Lau	AAT Asn 560	Gly	TCT Ser	G GA Gly	CTT (Leu (TAT Tyr 565	G AG Glu	1795
CCA Pro	ATG Met	GTT Val	G GG Gly 570	Glu	CAG Gln	CCC Pro	CCT Pro	CCA Fro 575	Leu	CTG Leu	G AG (G AG Glu	GAG A Glu A 580	AGA (GAG Glu	1843
ACA	Val	ATG Met 585	TGAC	CCAT	'AT C											1863

															GCGGC	CC 60
			r	1	TY P	CC G	Ta A	urg I	le A	la I	Pro :	Ser	Leu 10	λla	Leu	103
CTA Lev	CTC Leu	TGC Cys	. 6,3	CCA Pro	GTG Val	CTC Leu	AGC Ser 20	Ser	GCA Ala	TAT	GCC Ala	G CT	u Va	G GA 1 As	T GCG P Ala	113
G A C Asp	GAT Jak Jak Jak Jak Jak Jak Jak Jak Jak Jak	, , 447	TTT Phe	ACC Thr	AAA Lys	GAG Glu 35	GAA Glu	CAG Gln	ATT Ile	TTC	CTC Lev	ı Let	G CA	C CG	r GCC 7 Ala	204
CAG Gln 45	774	CAA Gln	TGT Cys	GAC Asp	AAG Lys 50	CTG Leu	CTC Leu	AAG Lys	GAA Glu	GTT Val 55	Leu	CAC His	ACI Thi	A GCA Ala	GCC A Ala 60	27.
AAC Asn	ATA Ile	ATG Met	GAG Glu	TCA Ser 65	GAC Asp	AAG Lys	G GC Gly	TGG	ACA Thr 70	CCA Pro	GCA Ala	TCI Ser	ACC Thr	TCA Ser 75	GGG Gly	300
A AG Lys	CCC Pro	AGG Arg	AAA Lys 80	GAG Glu	AAG Lys	GCA Ala	TCG Ser	GGA Gly 85	AAG Lys	TTC Phe	TAC Tyr	CCI	GAG Glu	Ser	AAA Lys	348
		95	vañ	AGI	PFO	THE	100	Ser	Arg	Arg	Arg	Gly 10	Arg 5	Pro	TGT Cys	396
	110	914	** *	vab	ASI	113	val	Cys	Lrp	Pro	Leu 120	Gly	Ala	Pro	Gly	444
125	, 44		.322	. 3 _	130	TGT Cys	-50	SD		11a 135	777	.\sp	Phe	Asn	His 140	490
2,0	G Z Ţ		VIG	145	arg	Arg	Cys	ASD	Arg 150	Asn	Gly	Ser	Trp	Glu 155	Val	54C
		GLY	160	ASII	Arg	ACG Thr	b	165	Asn	TYT	Ser	Glu	Cys 170	Leu	Lys	588
		175	vali	GIU	III	arg	180	arg	Glu	Val	Phe	Asp 185	Arg	Leu	Gly	636
ATG Met	ATC Ile 190	TAC Tyr	ACC Thr	GTG Val	GIY	TAC Tyr 195	TCC Ser	ATG :	ICT Ser	Leu	GCC Ala 200	TCC Ser	CTC Leu	ACG Thr	G TG Val	684

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GCT Ala 205	GTG Val	CTC Leu	ATC Ile	CTG Leu	GCC Ala 210	TAT Tyr	TTT Phe	AGG Arg	cgg Arg	CTG Leu 215	CAC His	TGC Cys	ACG Thr	CGC Arg	AAC Asn 220	732
TAC Tyr	ATC Ile	CAC His	ATG Met	CAC His 225	ATG Met	TTC Phe	c rc Leu	TCG Ser	TTT Phe 230	ATG Met	CTG Leu	CGC Arg	GCC Ala	GCG Ala 235	AGC Ser	780
ATC Ile	TTC Phe	GTG Val	AAG Lys 240	G AC Asp	GCT Ala	GTG Val	CTC Leu	TAC Tyr 245	TCT Ser	GGC Gly	TTC Phe	ACG Thr	CTG Leu 250	G AT Asp	G AG Glu	828
GCC Ala	GAG Glu	CGC Arg 255	CTC Leu	ACA Thr	GAG Glu	GAA Glu	GAG Glu 250	TTG Lau	CAC His	ATC Ile	ATC Ile	GCG Ala 265	CAG Gln	GTG Val	CCA Pro	876
CCT	CCG Pro 270	CCG Pro	GCC Ala	GCT Ala	GCC Ala	GCC Ala 275	GTA Val	GGC Gly	TAC Tyr	GCT Ala	GGC Gly 280	TGC Cys	CGC Arg	GTG Val	GCG Ala	924
GTG Val 285	ACC Thr	TTC Phe	TTC Phe	CTC Leu 290	TAC Tyr	TTC Phe	crs Leu	GCT Ala	ACC Thr 295	AAC Asn	TAC Tyr	TAC Tyr	TGG Trp	ATT Ile 300	ctg Leu	972
GTG Val	GAG Glu	G GG Gly	CTG Leu 305	TAC Tyr	TTG Leu	CAC His	AGC Ser	CTC Leu 310	ATC Ile	TTC Phe	ATG Met	GCC Ala	TTT Phe 315	TTC Phe	TCA Ser	1020
GAG Glu	AAG Lys	AAG Lys 320	TAC Tyr	CTG Lau	TGG	G GC Gly	TTC Phe 325	ACC	ATC Ile	TTT Phe	G GC Gly	TGG Trp 330	GGT Gly	CTA Leu	CCG Pro	1068
GCT Ala	GTC Val	TTC Phe	GTG Val	GCT Ala	GTG Val	TGG TYP 340	GTC Val	337	TTC Tal	AGA Arg	GCA Ala 345	ACC Thr	TTG Leu	GCC Ala	AAC Asn	1116
ACT Thr 350	GGG Gly	TGC Cys	TOG	GAT Asp	erg Leu 355	AGC Ser	TCC Ser	133 117	IAC His	AAG Lys 360	AAG Lys	TGG Trp	ATC Ile	ATC Ile	CAG Gln 365	1164
G TG Val	CCC Pro	ATC Ile	CTG Leu	GCA Ala 370	TCT Ser	GTT Val	GTG Val	CTC	AAC Asn 375	TTC Phe	ATC Ile	CTT Leu	TTT Phe	ATC Ile 380	AAC Asn	1212
ATC Ile	ATC Ile	cgg Arg	GTG Val 385	CTT Leu	GCC Ala	ACT Thr	AAG Lys	CTT Leu 190	og g A rg	G AG Glu	ACC Thr	Asn	GCG Ala 3 95	G GC Gly	CGG Arg	1260
TGT Cys	GAC Asp	ACC Thr 400	AGG Arg	CA G Gln	CAG Gln	TAC Tyr	CGG Arg 405	AAG Lys	CTG Leu	CTC Leu	Arg	TCC Ser 410	ACG Thr	TTG Leu	G TG Val	1308

	415				•	420		-1-	****	GTC Val	425	met	Ala	Leu	Pro	
430					435				J 211	ATC Tie 440	GIM	wer	His	Tyr	Glu 445	
				450			1		455		uld	TIE	Ile	Tyr 460	cya	
			465					470	115	λ GG A r g	Lys	ser	Trp 175	Ser	Arg	
		480					485	AL G	Lys	GCA Ala	Arg	ser 490	Gly	Ser	Ser	15;3
AGC Ser	495		•	-4		500		261	urs	****	505	val (Thr .	Asn	Val	1596
GGC (Gly 1 510		-			515		264	710	reu	520	rro %	urg I	Leu 1	Pro	Pro 525	1644
GCC A				530				Leu	535	GTÅ 1	als A	la I	Lys I	10 (Gly	1692
GCT (:	545			,	* • • •	.50	PFC	·al]	inr M	et A 5	la V 55	'al I	Pro	1740
AAG G Lys A		60	•			:	65		-!5	ser G	11 À 1	eu A 70	sp G	lu G	lu	1783
GCC TALL S	75				5	80			Leu 1	- eu G 5	35	lu G	ly T	rb e	lu	1835
ACA G Thr V 590																
TGGAC	agat agai	G GA	CCAA	GAAG	CCA	GTGT	TTG	GCTG	GTTG	TC T	ATTC	GGAT	CTC	GAC	CAGG	1945
AAGATA	3 A TO 2	m aa	GGAA	AATG	GAA	GTGG	ACG	AAGC	AGAG	AA GZ	l agg?	LAGAG	GTI	TTG	CAGG	2005
AATTAJ	-W.I.W.	r GT	TTCC	TCAG	TTG	gatg	ATG	AGG A	CACA	AG GA	\AGGC	:				2051

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1 MGAARIAPSLALLLCCTVLSSAYALVDADDVFTREZQIFLLHRAQAQCDX 50
           1 MGAPRISHSLALLLCCSVLSSVYALVDADDVITREEQIILLRNAQAQCEQ 50
     51 LLKEVLHTAANIHESDEGHTPASTSGEFRERASGEFYPESKEHEDVPTG 100
             51 REKEVER. VPELAESAKOW. . HSRSAKTKKEEPAEKLYPQAEESREVSOR 97
   101 SRRRGRPCLZEWDNIVCWPLGAPGEVVAVPCPDYIYDFNHKGZAYRRCDR 150
           the stationaria delicationalistations and the
     98 SRLODGFCLPEWDNIVCWPAGVPGRVVAVPCPDYFYDFNRKGRAYRRCDS 147
   151 NGSWEVVPGHNRTWANYSECLEFHTNETREREVFDRLGHIYTVGYSHSLA 200
          148 NGSWELVPGNNRTWANYSECVRPLTNETREREVPDRLGHIYTYGYSISLG 197
  201 SLTVAVUILAYFRRUHCTRNYIHHHHFLS7HLRAASIFVKDAVLYSGFTL 250
          198 SUTVAVUILGYFRRUHCTRNYIHHHUFVSFHURAVSIFIRDAVLYSGVST 247
  251 DEAERLTEEELHIJAQVPPPPAAAAVGYAGCRYAVTFFLYFLATNYYWIL 300
         148 DEIERITEEELRAFTE... PPPADKAGFVGCRVAVTVFLYFLTTNYYWIL 294
  301 VEGLYLHSLIFMAFFSERKYLWGFTIFGHGLFAVFVAVWVGVRATLANTG 350
         195 VEGLYLHSLIFMAFFSERKYLWGFTLTGWGLFAVFVAVWVTVRATLANTE 344
 351 CHOLSSCHRRWIIQVPILASVVLNEILFINIIRVLATRLRETNAGRCDTR 400
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 345 CHOLSSGNERWIIQUPILAAIUUNFILFINIIRVLATELRETNAGRCDTR 394
 401 GOYRKLLRSTLVLVPLFGVHYTVFMALPYTEVSGTLWQIQMHYEMLFNSF 450
         395 GQYRKLLKSTLVLMPLFGVHYIVFMATPYTTVSGILWQVQRHYEMLFMSF 444
451 GGFFVAIIYCFCMGEVQAZIRKSWSRWTLALDFKRKARSGSSSYSYGPMV 500
        445 CGFFVAITYCFCNGEVQAEIRKSWSRWTLALDFRRKARSGSSTYSYGPHV 494
501 SHTSVTHVGFRAGLSLPLSPRLPP...ATTHGHSQLPGHAKPGAPATETE 547
         .... ....
495 SHISVINVGERGGLALSLSPRLAPGAGASANGBROLPGYVKHGSISENSL 544
548 TLFVTMAVPRODGFLNGSCSGLDEEASGGARFPPLLGEGWETVM. 591
545 PSSGPEPGTXDDGYLNG..SGLYEPMYG.ECPPPLLEZERETWN 586
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Gap Weight: 3.000 Average Match: 0.540 Langth Weight: 0.100 Average Mismatch: -0.396

Quality: 712.2 Langth: 595
Ratio: 1.215 Japs: 6
Percent Similarity: 87.113 Percent Identity: 77.835
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RIS	MGAARIAPS	L ALLLCCPVL	S SAYALVDAD	D VETREZOIS	L LERAQAQCE	
Oko	UNAFRIDAD	L ALLLLESVI	S SUYALUNAN	n utterbentt	'	
Okh	MGAPRISHS	L ALLLCCSVL	S SYYALVDAD	D VITREEOII	L LRNAQAQCE	
		A			- GRENONYCE	Q 50
R15	LLKEVLHTA	A NIMESDKOW	T PASTSGEPR	T FEASCEPYS	E SKENKOVPT	
Oko	UPVEATV.A	r clarsakow	. STREATT	T FTDARWTVS	A	
Okh	RLKEVLR.V	P ELAESAKOW	MEDGARTE	r culverril	Q AZZSRZVSD Q AZZSRZVSD	R 97
				r capacally	A VEEZMEAZD	R 97
	•	•				
215	SARRGERCT	2 FWDNIUCWD			•	
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Oko		, iranlatiki	A YIMMHI PUCH	' WIDLUCTPY	P	
Okh	2011445	IL VERTUE LEE	YIRMHLEVSE	MLRAVSIPI	DAVLYSGVS	247
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R15	DEAERLTEEE	LHIIAQVPP	PAAAAVGYAG	CRVAVTERLY	FLATNYYWII	200
Oko	OCICALICE	LAAFTE	PPARKACEUR			
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R15	VEGLYLHSLI	FMAFFSEKKY	LWGFTIFGWG	LPAUPUAULU	GVRATLANTG	
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R15	CWDLSSGHKK	WIIOVPILAS	VVI.NPTT.FTN	TTRUTATET 9	ETNAGRODTR	
Oko		MILLIANT	TUUNIPIT PIN	7 7 TOTT 1 MET 0		
Okh	CWDLSSGNKK	WIIOVPILAA	IVUNETT. FTR	TIBUT LTEF	ETNAGRODTR	394
			B		LIMAGECUTE	394
						
R15	QQYRKLLRST	LVLVPLFGVR	YTTTHALDYT	FUSCETWOLD	MHYEMLINSI	
Oko	QQYRKLLKST	LVLMPLEGVE	VIVENATOVE	CISCILIONO	MEYEMLENSE	450
Okh	COYRELLEST	LVLMPLEGVH	VIVENATOVE	TARETTHOUGH	ABYEMLENSE ABYEMLENSE	444
				TARRITAGAG		444
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R15	OGFFVALLYC	FCNGEVOART	3 E CWCDW#1 1		SSSYSYGPMV	
Oko	OGFFVAIIYC	ECNGEVOAFT	VECUCDUTT N	LOTARAMAG	SSTYSYGPHV	500
Okh	OGFFVALLYC	FCNGEVOART	ALCHCAMMA F	LDINAKAKSG	SSTYSYGPHV	494
	J		VYSHOWITH	LUIKKKAKSG	SSTYSYGPMV	494
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R15	SHTSVTNVCP	RAGISTATES	2122	VCREO. Ber-		
Oko	SHISVINGE	PGG: 1: c: cn	READCECT.	NGBSQLPGEA	KPGAPATETE	547
	SHTSVTNVGP SHTSVTNVGP				KHGSISENSL	544
			APCPSA	23		515
R15	TEPVTMAUDE	DOGETAGECE	C1 BBB1 444-			
Oko	TLPVTMAVPK 255GPFPGTK	DDGYLNGSCS	CLUEEASGSA	KEPPLLQEGW	EIVH	591
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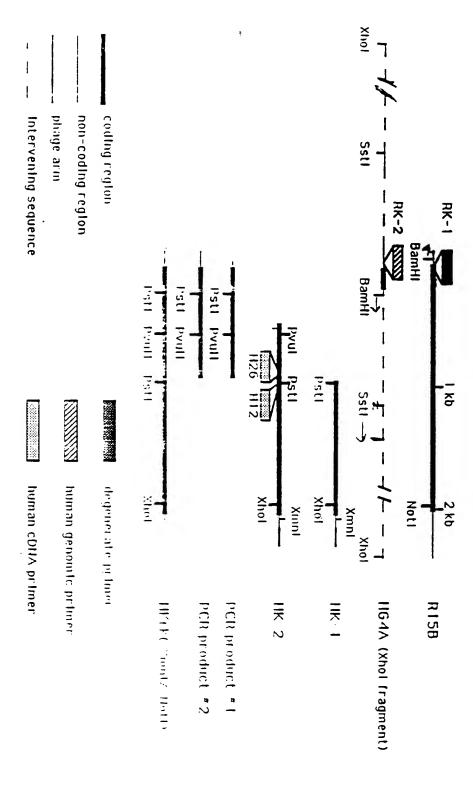
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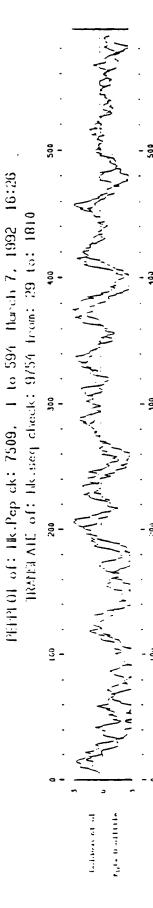
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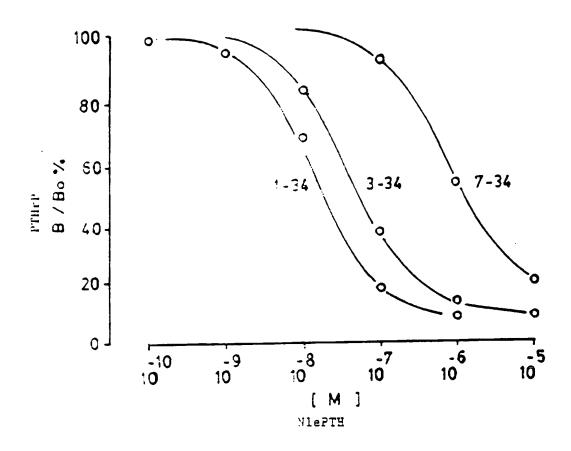
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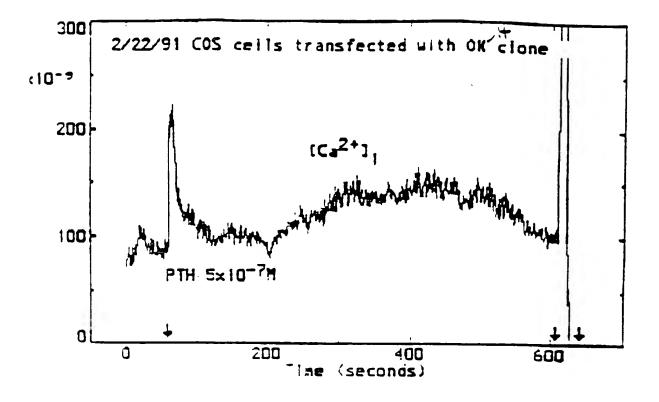


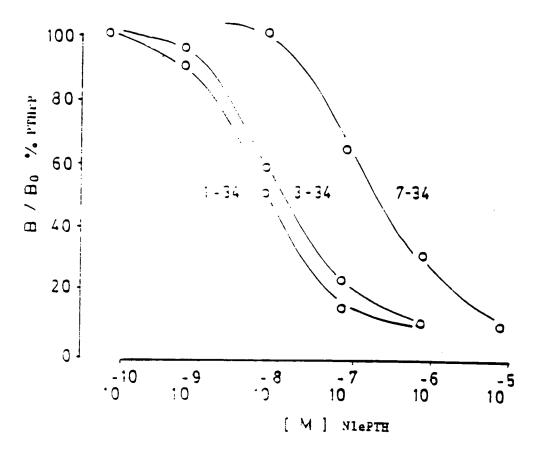


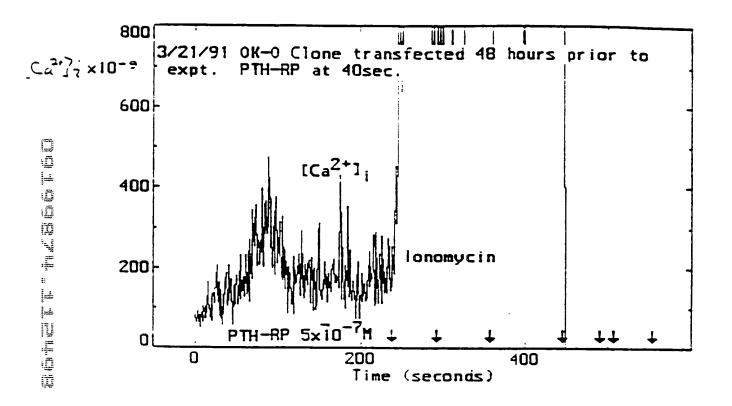
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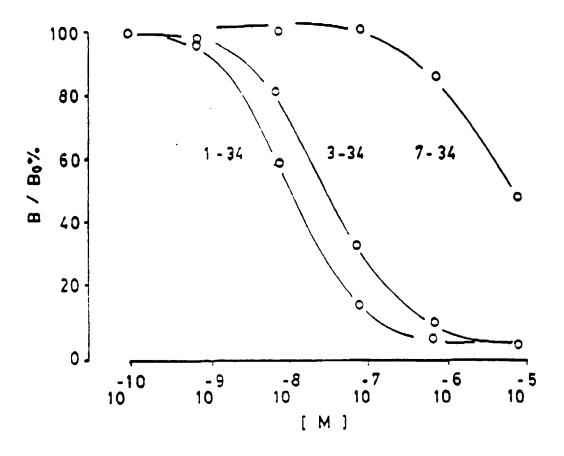
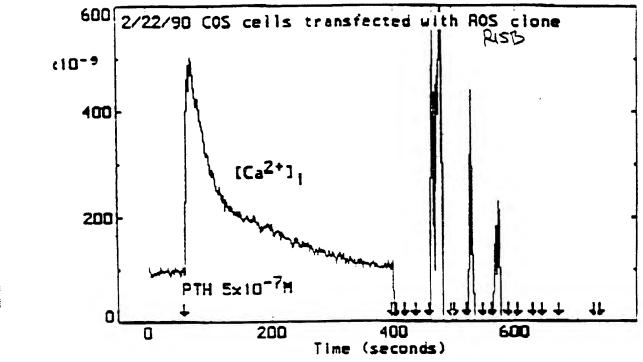
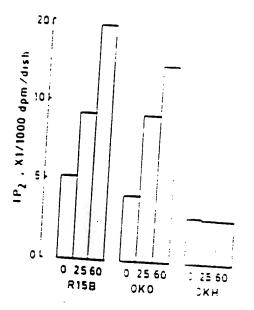
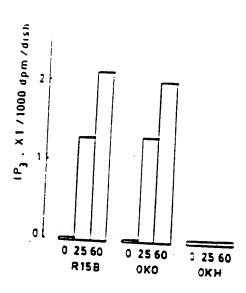


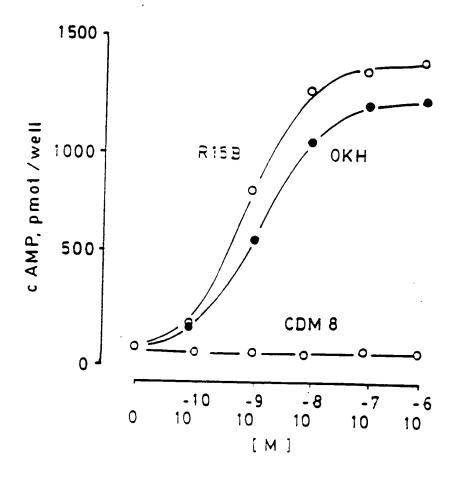
FIG. 13

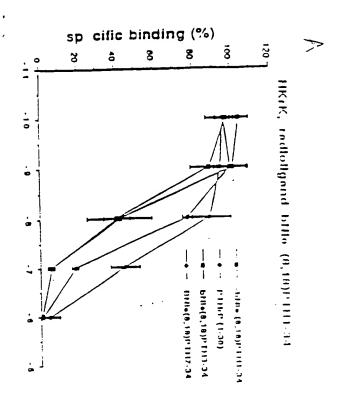
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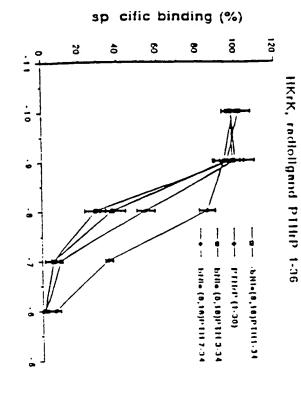


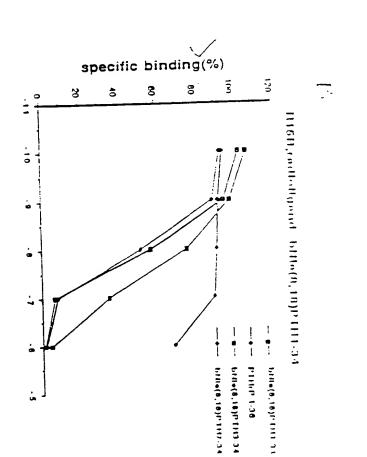












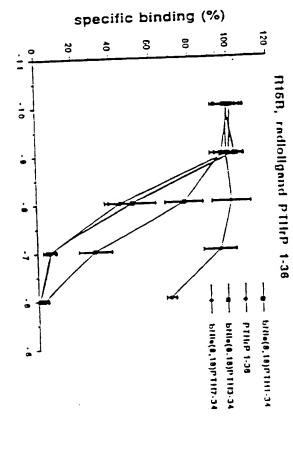
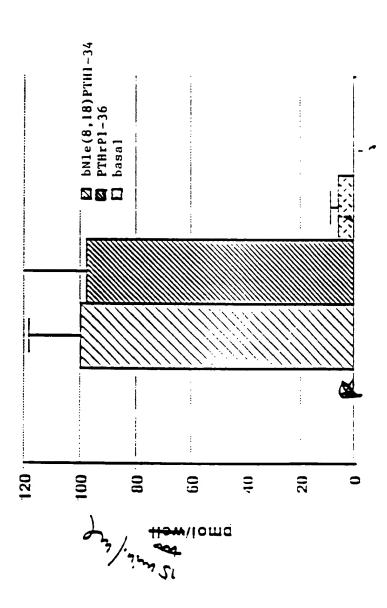


Fig. 1



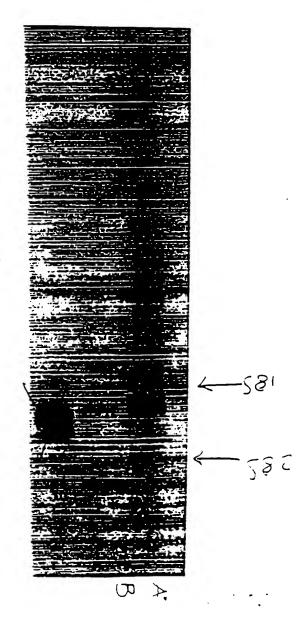
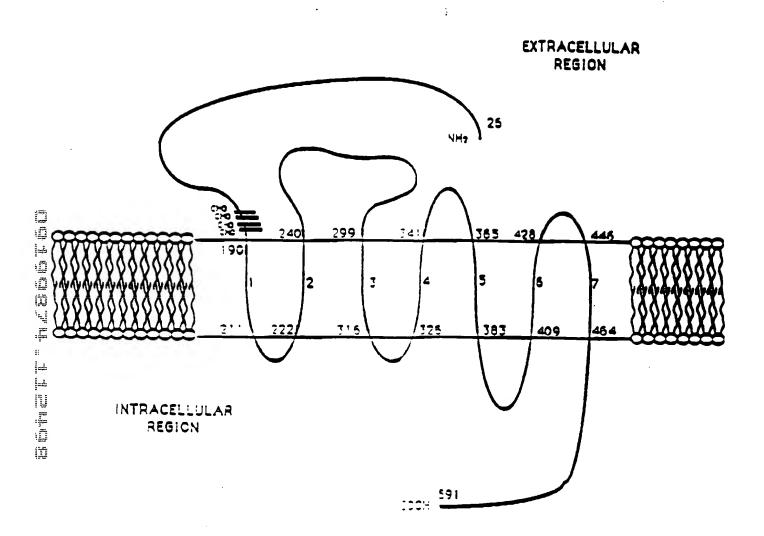


Fig .9



RAT BONE PTH/PTHrP RECEPTOR



AMING ACID SEQUENCE OF 7 PUTATIVE TRANS-MEMBRANE REGIONS

